theoretical biologist, and to get her interested in our problems. Around the turn of the millennium, a sparkling collaboration ensued which involved several very talented individuals from her group. With this collaboration, we could formulate our questions in testable hypotheses because they can be simulated. We have gone that way ever since. We still work together, as can be seen from our recent papers. In the meantime, collaborative links have spread to make up different partner groups with whom we maintain very valuable contacts.

What can biologists gain from working with theorists? The researchers directly working on projects that involve modelling get a good feeling of the power of a formal statement of their problems. This may well change the way in which they plan their experiments and will shape their intuition for meaningful but as-yet hard to understand data. But also group members not directly linked to modelling will be exposed to different ways of approaching a problem — they are also educated in a 'next generation' type of biology. Finally, we get way better models to explain our observations!

What are the next challenges in plant developmental biology? We still need to decipher the exact mechanisms for cell polarization. The role of mechanical forces in plant development must be explored in much greater depth. And finally, plants use development to respond to the environment, in other words, to 'behave'. We are only just now discovering the numerous connections between developmental programs and environmental cues (light, nutrients, stress, pathogens, mutualists). These connections must define the 'intelligence' of plants which make them successful colonizers of our planet — and help them sustain our survival on it.

Can you give an example of that intelligence? I have ground elders in my garden (*Aegopodium podagraria*). They have chosen to live there and no act of human intelligence has been able to undo that fact.

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Quick guide

P granules

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What are they? P granules are the *Caenorhabditis elegans* 'germ granules', a class of perinuclear RNA granules specific to the germline. The defining components of P granules are two classes of RNA-binding proteins: the RGG-domain proteins, PGL-1 and PGL-3; and the DEAD-box proteins, GLH-1–4 (also related to *Drosophila* Vasa).

Why are they called P granules? P granules get their name from the P lineage, the embryonic lineage that gives rise to the germline. P granules segregate asymmetrically with the P lineage during embryogenesis and are maintained in germ cells throughout life (except for mature sperm). P granules should not be confused with P-bodies (also called processing bodies), a different class of RNA granules present in all cells.

What holds P granules together? Like other RNA granules, P granules are not membrane bound. Granule assembly depends on self-interaction domains in the PGL proteins, and the localization of P granules to nuclei is promoted by FG repeats in the GLH proteins. Despite their structural role, PGL and GLH proteins are highly mobile and readily exchange with the surrounding cytoplasm. When pushed by a needle, P granules deform and 'drip' off (i.e. dissociate from) nuclei. In the P lineage, P granules shrink, grow and fuse at each cell division. These properties have suggested that P granules are liquid droplets, held together by low-affinity interactions that cause P-granule proteins to undergo phase separation from the bulk cytoplasm.

What else is in P granules? Because P granules sit on nuclear pores, most mRNAs transcribed in germ cells likely pass through a P granule on their way to the cytoplasm. Consistent with a role in mRNA surveillance, several members of the Argonaute family of RNA regulators are enriched in P granules, including: CSR-1, which protects germline mRNAs from silencing; and PRG-1 and WAGO-1, which silence transposable elements and foreign genes. The Vasa-like protein RDE-12 associates with WAGO-1 in P granules and is required for siRNA amplification, which has been proposed to occur in 'mutator loci' adjacent to the P granules. A link between Vasa, Argonautes and the amplification of small RNAs has also been observed in the perinuclear 'nuage' of *Drosophila*, suggesting a possible conserved role in the synthesis of small RNAs.

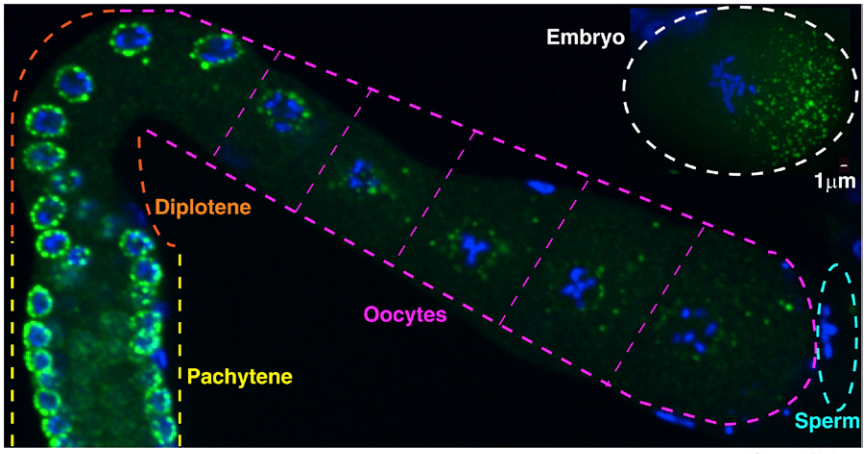

Figure 1. P granules.
P granules (detected using the OIC1D4 antibody) in an adult hermaphrodite gonad. P granules are perinuclear in germ cells in the pachytene and diplotene stages of meiosis and become progressively more cytoplasmic in growing oocytes. The inset at top right shows cytoplasmic P granules (detected with an anti-GLH-2 antibody) in an embryo in the first mitotic prophase: these P granules are enriched on the posterior side. P granules are in green, and DNA is in blue. Scale bar = 1 μm. (Image: Jennifer T. Wang.)

What happens when you get rid of P granules? Mutants that fail to partition P granules to the P lineage are viable and fertile, suggesting that P granules are not essential to distinguish soma from germline in embryos. Mutations in individual P-granule components lead to sterility at high temperature and impaired translational control of at least some mRNAs. What happens when germ cells lack all P granules, however, has been hard to determine due to functional redundancy among P-granule components. A recent study found that simultaneous depletion of PGL-1, PGL3, GLH-1 and GLH-4 gives rise to germ cells that occasionally express somatic markers and form neurite-like extensions. An attractive possibility is that P granules preserve the totipotency of the germline by silencing somatic differentiation programs until fertilization.

Where can I find out more?

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Marine mammals trace anthropogenic structures at sea

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On land, species from all trophic levels have adapted to fill vacant niches in environments heavily modified by humans (e.g. [1]). In the marine environment, ocean infrastructure has led to artificial reefs, resulting in localized increases in fish and crustacean density [2]. Whether marine apex predators exhibit behavioural adaptations to utilise such a scattered potential resource is unknown. Using high resolution GPS data we show how infrastructure, including wind turbines and pipelines, shapes the movements of individuals from two seal species (*Phoca vitulina and Halichoerus grypus*). Using state-space models, we infer that these animals are using structures to forage. We highlight the ecological consequences of such behaviour, at a time of unprecedented developments in marine infrastructure.

Evidence for use of anthropogenic structures at sea by apex predators is limited and based on non-individualised presence data from acoustic or visual studies focused on single structures or complexes [3]. To understand this issue, we need high resolution data on fine-scale movement and activity patterns of individual animals in relation to both point (e.g. wind turbines) and linear structures (e.g. pipelines). Such data are now available from animal-borne GPS tracking devices (GPS/GSM tags, Sea Mammal Research Unit). Tags were deployed on harbour and grey seals on the British and Dutch coasts of the North Sea (Supplemental information). Both species alternate foraging trips at-sea, lasting from a few days to a month, with visits to land to haul-out.

We recorded 11 harbour seals within two active windfarms: Alpha Ventus, Germany and Sheringham Shoal, south-east United Kingdom. In the north-east Netherlands, four of 96 individuals tagged in 2010 and 2011 (tag duration: 25–161 days) entered Alpha Ventus (constructed in 2009 and operational from 2010). Two of these four showed striking grid-like patterns of movements as they concentrated their activity at individual turbines (Figure 1). In 2012, while some turbines were operational, seven of the 22 individuals tagged in south-east England entered Sheringham Shoal (construction: 2010–2012); one did so on each of its 13 trips and showed similar grid-like movement patterns (Supplemental movie S1).

Movements of both grey and harbour seal individuals showed associations with subsea pipelines (Supplemental information). In 2008, of ten grey and six harbour seals tagged in south-east Scotland, one of each species associated with pipelines. Of 138 harbour seals tagged in the north-east Netherlands (2009–2011), two encountered a section of pipeline and both followed it on multiple trips for up to ten days at a time (see Figure S1). In addition, two of 22 seals tagged elsewhere in the Netherlands were also recorded following pipelines.

The data strongly suggest that these structures were used for foraging and the directed movements show that animals could effectively navigate to and between structures. Area restricted searching, characterized by high sinuosity and reduced horizontal speed, has been used to identify likely foraging in seals [4]. Using state space models [4], we found that the three animals that showed a grid-like movement pattern concentrated their foraging effort in the windfarms (Supplemental information). Furthermore, once within the windfarm area, the probability of foraging significantly increased towards individual structures for the two seals that spent the majority of their time near the turbines (Figure 1). When following linear structures, high sinuosity associated with area restricted searching should not be expected by default. However, within 100 m of the pipelines, the measurements of speed were similar to the foraging speed distribution estimated by the state-space model (Supplemental Figure S1).

The finding that a proportion of seals adjust their behavior to make use of anthropogenic structures raises questions regarding the attributes of these individuals and the ecological consequences of such behavior. The individuals utilizing structures often